

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/785,532DATE: 07/10/97  
TIME: 18:42:55

INPUT SET: S18901.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

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## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Gray, Joe W.  
Collins, Colin  
Hwang, Soo-In  
Godfrey, Tony  
Kowbel, David  
Rommens, Johanna

(ii) TITLE OF INVENTION: Genes From the 20q13 Amplicon and Their  
Uses

(iii) NUMBER OF SEQUENCES: 55

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, 8th Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/785,532  
(B) FILING DATE: 17-JAN-1997  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/731,499  
(B) FILING DATE: 16-OCT-1996

## (viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/680,395  
(B) FILING DATE: 15-JUL-1996

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Quine, Jonathan A.  
(B) REGISTRATION NUMBER: P-41,261

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47 (C) REFERENCE/DOCKET NUMBER: 023070-068920US  
48  
49 (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: (415) 576-0200  
51 (B) TELEFAX: (415) 576-0300  
52  
53  
54 (2) INFORMATION FOR SEQ ID NO:1:  
55  
56 (i) SEQUENCE CHARACTERISTICS:  
57 (A) LENGTH: 3000 base pairs  
58 (B) TYPE: nucleic acid  
59 (C) STRANDEDNESS: single  
60 (D) TOPOLOGY: linear  
61  
62 (ii) MOLECULE TYPE: cDNA  
63  
64  
65 (ix) FEATURE:  
66 (A) NAME/KEY: -  
67 (B) LOCATION: 1..3000  
68 (D) OTHER INFORMATION: /note= "cDNA clone 3bf4 of 3kb  
69 transcript of tyrosine kinase gene A6"  
70  
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
72  
73 CCGCCGGCCG GGGCGCCTGG CTGCACTCAG CGCCGGAGCC GGGAGCTAGC GGCCGCCGCC 60  
74  
75 ATGTCCCACC AGACCGGCAT CCAAGCAAGT GAAGATGTTA AAGAGATCTT TGCCAGAGCC 120  
76  
77 AGAAATGGAA AGTACAGACT TCTGAAAATA TCTATTGAAA ATGAGCAACT TGTGATTGGA 180  
78  
79 TCATATAGTC AGCCTTCAGA TTCCTGGGAT AAGGATTATG ATTCCCTTTGT TTTACCCCTG 240  
80  
81 TTGGAGGACA AACAACCATG CTATATATTA TTCAGGTTAG ATTCTCAGAA TGCCAGGGA 300  
82  
83 TATGAATGGA TATTCATTGC ATGGTCTCCA GATCATTCTC ATGTTCTGCA AAAAATGTTG 360  
84  
85 TATGCAGCAA CAAGAGCAAC TCTGAAGAAG GAATTTGGAG GTGGCCACAT TAAAGATGAA 420  
86  
87 GTATTTGGAA CAGTAAAGGA AGATGTATCA TTACATGGAT ATAAAAAATA CTTGCTGTCA 480  
88  
89 CAATCTTCCC CTGCCCCACT GACTGCAGCT GAGGAAGAAC TACGACAGAT TAAAATCAAT 540  
90  
91 GAGGTACAGA CTGACGTGGG TGTGGACACT AAGCATCAAA CACTACAAGG AGTAGCATT 600  
92  
93 CCCATTTCTC GAGAAGCCTT TCAGGCTTTG GAAAAATTGA ATAATAACA GCTCAACTAT 660  
94  
95 GTGCAGTTGG AAATAGATAT AAAAAATGAA ATTATAATTT TGCCCAACAC AACAAATACA 720  
96  
97 GAACTGAAAG ATTTGCCAAA GAGGATTCCC AAGGATTCAG CTCGTTACCA TTTCTTTCTG 780  
98  
99 TATAAACATT CCCATGAAGG AGACTATTTA GAGTCCATAG TTTTATTTTA TTCAATGCCT 840



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154		
155	TTAAACATGC AAAATAACTG ACAATAATGT TGCACCTTGTT TACTAAAGAT ATAAGTTGTT	2520
156		
157	CCATGGGTGT ACACGTAGAC AGACACACAT ACACCCAAAT TATTGCATTA AGAATCCTGG	2580
158		
159	AGCAGACCAT AGCTGAAGCT GTTATTTTCA GTCAGGAAGA CTACCTGTCA TGAAGGTATA	2640
160		
161	AAATAATTTA GAAGTGAATG TTTTCTGTGA CCATCTATGT GCAATTATAC TCTAAATTCC	2700
162		
163	ACTACACTAC ATTAAAGTAA ATGGACATTC CAGAAATATAG ATGTGATTAT AGTCTTAAAC	2760
164		
165	TAATTATTAT TAAACCAATG ATTGCTGAAA ATCAGTGATG CATTTGTTAT AGAGTATAAC	2820
166		
167	TCATCGTTTA CAGTATGTTT TAGTTGGCAG TATCATACCT AGATGGTGAA TAACATATTC	2880
168		
169	CCAGTAAATT TATATAGCAG TGAAGAATTA CATGCCCTTCT GGTGGACATT TTATAAGTGC	2940
170		
171	ATTTTATATC ACAATAAAAA TTTTCTCTCT TTAACAAAAA AAAACAAGAA AAAAAAAAAA	3000
172		
173		

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: /note= "cDNA clone 1b11 of 3.5kb transcript"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

193		
194	TGGAAGCTGT CATGGTTACC GTCTCTAACG TTGGACTCTT AAGAAAATGA TTATTCCTGG	60
195		
196	TTTCTAGACA GGCCAAATGT AATTCACCTA CGTGGCAGAT TAAAGAGGTG GGCTTACTAG	120
197		
198	ATTTGATTGG GTATTGAGCA TGCTCTGAAT GACAGTCCCC AAAAAGGACC TCTTATCCGT	180
199		
200	TCTTCCCCCTT GGGGAAGGGC TTTTGCCACT TCCATGTCAA TGTGGCAGTT GAGCTTGAA	240
201		
202	ATTGGTGCGT TGTACAACAT AAGCATTACT TCTCCAAGAT GTGCCTGTGT AGAAATGGTC	300
203		
204	ATAGATTCAA AACTGTAGCT ACTATGTGGA CAGGGGGGCA GCAAGGACCC CACTTTGTAA	360
205		

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/785,532

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206	AACATGTTTT GGGGGAATGT TTTGTTTTTC ATTTTCTTAT TACCTGGCAA AATAATCCAG	420
207		
208	GTGGTGTGTG AGTCACCAGT AGAGATTATA AAGTCCAAGG AAGTAGAATC AGCCTTACAA	480
209		
210	ACAGTGGACC TCAACGAAGG AGATGCTGCA CCTGAACCCA CWGAAGCGAA ACTCAAAAGA	540
211		
212	GAAGAAAGCA AACCAAGAAC CTCTCTGATG RCGTTTCTCA GACAAATGGT AAGCCCCTTA	600
213		
214	CTTCCAGTAT AGGAAACCTA AGATACCTAG AGCGGCTTTT GGGAACAATG GGCTCATGCC	660
215		
216	ACAGGTAGTA GGAGACATAA TTGTAGCTGG TGTGTATGGA ATGTGAATGG AATATGGATT	720
217		
218	GCG	723
219		
220		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1507
- (D) OTHER INFORMATION: /note= "cDNA clone cc49 of 6-7kb transcript with homology to C2H2 zinc finger genes"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

241		
242	GCAGGTTGCT GGGATTGACT TCTTGCTCAA TTGAAACACT CATTCAATGG AGACAAAAGAG	60
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244	CACTAATGCT TTGTGCTGAT TCATATTTGA ATCGAGGCAT TGGGAACCCCT GTATGCCTTG	120
245		
246	TTTGTGGAAA GAACCAAGTGA CACCATCACT GAGCTTCCTA AAAGTTCGAA GAAGTTAGAG	180
247		
248	GACTATACAC TTTCTTTTGA ACTTTTATAA TAAATATTTG CTCTGGTTTT GGAACCCAGG	240
249		
250	ACTGTTAGAG GGTGAGTGAC AGGTCTTACA GTGGCCTTAA TCCAACCTCA GAAATTGCCC	300
251		
252	AACGGAACTT TGAGATTATA TGCAATCGAA AGTGACAGGA AACATGCCAA GTCAATCCCT	360
253		
254	CTTAATGTAC ATGGATGGCC AAGAGTGATT GGCAGCTCTC TTGCCAATCC GATGGAGATG	420
255		
256	GAGATGCCTT GTCAATGAAA GGGCCCNCTG TTGTCAATTC CGAGCTACAC AAAGAAAAAA	480
257		
258	ATGTCAATCC GAATCGAGGG GAATATGCCC TTGGATTGCA TGTCTGCAG CCAGACCTTC	540

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/785,532**

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